Reconstructing Metabolic Images from Hyperpolarized ^{13}C 3T MRSI data using AMARES for Reduced FID Sampling

P. Pels[1], M. L. Zierhut[1,2], I. Park[1,2], Y-F. Yen[3], A. Chen[1,2], R. Bok[1], V. Zhang[1], M. Albers[1,2], D. Vigneron[1], J. Kurhanewicz[1], R. Hurd[3], and S. J. Nelson[1]

[1]Radiology, University of California, San Francisco, San Francsico, CA, United States, [2]UCSF/UCB Joint Graduate Group in Bioengineering, San Francsico, CA, United States, [3]GE Healthcare, Menlo Park, CA, United States

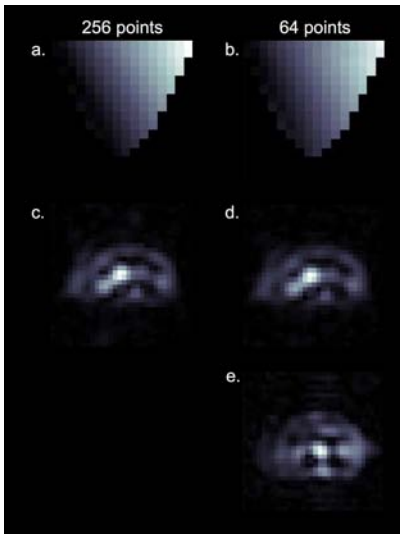
Introduction

Hyperpolarization via dynamic nuclear polarization can improve the SNR of ^{13}C labeled probes by a factor of 10,000 [1]. This greatly enhanced SNR and the long T_1 relaxation of the compound can be used in ^{13}C MRSI to reduce the number of acquired FID samples. To reconstruct the metabolite images, the intensities of the different metabolites in different voxels need to be estimated. This can be obtained from peak height estimation in the frequency domain or by using a Dixon based method proposed by Reeder et al. [2]. This abstract describes the use of the time domain fitting algorithm AMARES [3] to obtain metabolite intensities to generate the metabolic images. The goal of this study was twofold: (1) to determine the minimal FID length necessary to obtain robust image reconstruction and (2) to verify the effect on overall SNR and optimal acquisition timing in the context of metabolic conversion rates of the injected pyruvate.

Methods

SIMULATIONS

Model spectra for alanine, pyruvate and lactate were simulated with a 500 Hz and a 5000 Hz bandwidth based on an *in vivo* hyperpolarized ^{13}C rat spectrum acquired at 3T. Bandwidths corresponded to an EPSI and a MRSI acquisition. Simulated metabolic images were generated by a linear combination of metabolite model spectra and a metabolite specific gradient mask (Figure 1a.). Noise was added to the simulated MRSI's to simulate an SNR of 8, 16 and 24 for pyruvate in the center voxel of the simulated MRSI with the lowest SNR corresponding to the *in vivo* CSI SNR.



DATA ACQUISITION

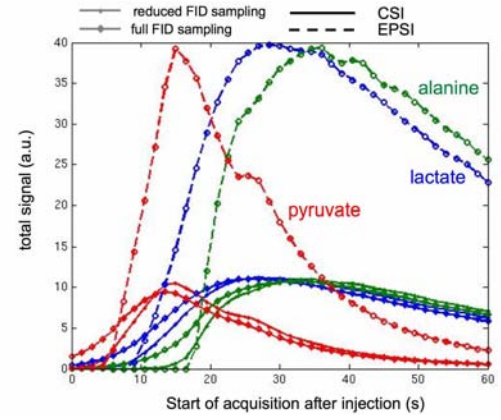
A 5000 Hz bandwidth hyperpolarized ^{13}C MRSI of was acquired on 8 rats on a 3T GE Signa Excite scanner using a dual-tuned rat coil with TR of 80 ms and 256 FID samples. Total scan time was 20.5 seconds. Spectral array dimensions were 16 x 16 (FOV = 90 x 90 mm) with a slice thickness of 40 mm resulting in voxels with a nominal spatial resolution of 1cc. One dataset was acquired with the same settings but only acquiring 64 datapoints and with a TR of 36 ms, total scan time 9.2 seconds.

DATA PROCESSING

Both simulations and *in vivo* data were quantified using AMARES, a model based time domain fitting algorithm. The image reconstruction based on the FID was consecutively done with 256, 128, 64, 32 and 16 points for the 5 kHz bandwidth data and with 50, 25, 13, 7 and 4 points for the 500 Hz bandwidth data. The following prior knowledge was imposed during quantification of the alanine, pyruvate and lactate peaks: all linewidths equal, frequencies constrained within a 20 Hz region around the frequency starting point and no constraints on individual phases. The estimated metabolite intensities were used to generate the metabolic images.

DYNAMICS

To analyse the effect of the different sampling times on the overall image SNR of the images, the overall signal of a 16x16 MRSI and EPSI acquisition was simulated using dynamic conversion curves. These curves were obtained from a series of non-localized spectra from a 40 mm slice through the kidneys with a temporal resolution of 3 seconds. These curves contain the effects of T_1 relaxation of the hyperpolarized compound and the metabolic conversion of pyruvate in alanine and lactate. The curves were corrected for the small flip angle excitation. Based on the sampling timings of the different acquisitions, the total signal intensity was calculated as the sum of interpolated values from the different dynamic curves.



Results & Discussion

Simulations showed high (>0.99) correlations between the estimated and the original amplitudes when more than 32 / 7 points were used for the 5kHz / 500Hz bandwidth simulations. This corresponds with a spectral resolution of about 78.1 / 71.4 Hz/point. Figure 1a. and 1b. show the reconstructed simulated alanine images using 256 and 64 points respectively. Images for pyruvate and lactate were reconstructed with same accuracy. When less points were used in the reconstruction, the correlation decreased. Therefore the metabolic images were reconstructed using 64 FID points. Changing the SNR did not change our simulations findings, which could be an indication that the accuracy of AMARES is no longer determined by the SNR but by the theoretical lower bound on the accuracy of amplitude estimates, also known as Cramer-Rao bounds. This was confirmed by the calculated Cramer-Rao bounds which increased from 13% to 280% when the number of points was reduced from 64 to 32 points. Figure 1c. and 1d. show a reconstructed *in vivo* lactate image using the full FID and using 64 points in the reconstruction. Correlation between the amplitudes of the images reconstructed with 256 points and those using only 64 points was on average over all the 8 datasets 0.98, 0.70 and 0.95 for lactate, alanine and pyruvate respectively, confirming the results from the simulations. Figure 1e. shows the reconstructed pyruvate image from the dataset in which only 64 points were acquired, proving the feasibility of reducing the FID sampling length by a factor 4, leading to a total acquisition time of 9.2 seconds. Figure 2 shows the normalized total signal intensities for pyruvate, alanine and lactate as a function of the acquisition start times after administration of the hyperpolarized pyruvate for MRSI (solid, diamond marker), reduced FID sampled MRSI (solid, diamond marker) and an EPSI sequence (dashed). Reducing the TR of the acquisition increases the total signal that can be acquired and also shifts the timing of the optimal acquisition window, which is different for the different metabolites. The average signal increase for the MRSI sequence was 10.4 ± 1.8 %, 2.3 ± 0.5 % and 3.2 ± 0.7 % for pyruvate, lactate and alanine respectively with reduced FID sampling. Because of the much faster acquisition of the 16x16 EPSI slice (1.4 sec) and more optimal excitation scheme, there was a total signal increase for the simulated EPSI acquisition of 362.0 ± 15.7%, 313.0 ± 6.1% and 315.8 ± 3.9% compared to the standard MRSI acquisition. Simulations showed that a 3D 16x16x8 3D EPSI sequence acquired in 11 sec on average has a total signal intensity of 22.6 a.u. per slice or 57.6 % of the total intensity of a single 16x16 EPSI slice.

Conclusion The results of simulations and an *in vivo* case using data acquired at 3T show that reconstructing metabolite images with a reduced number of FID samples is possible. Simulations show that this reduced FID sampling increases SNR. As acquisition time is such a critical factor in acquiring signals from hyperpolarized compounds the use of AMARES or other time domain fitting algorithms is likely to be important for designing acquisition protocols that can provide quantitative 2-D and 3-D metabolite images.

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